C.F.R. §§ 1.825(a) and 1.821(c) and a copy of the Substitute Sequence Listing in computer readable form as required by 37 C.F.R. § 1.825(b) and § 1.821(e).

As required by 37 C.F.R. §1.825(b), Applicants' Attorney hereby states that the content of the Substitute Sequence Listing in paper form and the computer readable form of the Substitute Sequence Listing are the same and, as required by 37 C.F.R. §1.825(a), also states that the submission includes no new matter.

Please amend the above-identified application as follows:

In the Specification

Please replace the Sequence Listing filed on July 23, 2001 (sheets 1/8 through 8/8) with the attached Substitute Sequence Listing (sheets 1/9 through 9/9), comprising SEQ ID NOS: 1-23, in the above-referenced application.

Please replace the paragraph at page 5, lines 1 through 22, with the following paragraph:

Figure 2 shows the exonic structure of the Xp GK gene and location of sequence polymorphisms. The first PAC clone, RPCI-5.931_C_24, containing exons 1 to 12 was used as sequencing template for exons 9, 10 and 11. An insert of 394 base pairs (bp) was found after the 36th nucleotide of exon 9, suggesting that the originally described exon actually consists of two exons (9A and 9B). These exons are 36 and 68 bases in length, respectively, and the corresponding intron-exon boundaries have the expected consensus splice site sequence as shown. When the sequence obtained for intron 10 was aligned with the published cDNA sequence, it was discovered that the splice junctions had been incorrectly defined, so that the last 12 bases of exon 10 were in fact encoded by exon 11. Furthermore, when the entire intron was sequenced, rather than being greater than 8 kilobases (kb) in length as originally believed, it was found to be 456 bp. Using primers located in introns 16 and 18 (forward and reverse primers, respectively), an amplicon was generated from the second clone, RPCI-5.1150_E_8 and then sequenced to determine the sequence of the 3' end of intron 7. Boxes show each exon and its length in base pairs (intron length not drawn to scale). Primers used to amplify each exon are